

SEQUENCE LISTING

<110> ENDO, NOBORU
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AKIYOSHI, MIHO
YOSHIDA, YASUKO
OHSUMI, CHIEKO
IGARASHI, DAISUKE

<120> GENE CAPABLE OF IMPARTING SALT STRESS RESISTANCE

<130> 279689US0XPCT

<140> 10/553,124

<141> 2005-10-14

<150> PCT/JP04/05403

<151> 2004-04-15

<150> JP 2003-113194

<151> 2003-04-17

<150> JP 2004-075932

<151> 2004-03-17

<160> 17

<170> PatentIn version 3.3

<210> 1

<211> 1554

<212> DNA

<213> Seashore Paspalum

<220>

<221> CDS

<222> (131)..(1222)

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gacggcgag atg ggc atc ggc ggc ggc gag gcc ggc ggc ggc gga ggc ggc 169
Met Ala Ile Gly Gly Ala Glu Ala Gly Gly Gly Gly Ala
1 5 10

ggg gcc agc ggc cgc agc gtg ctg gtg acg ggc ggc ggc ggc ttc atc 217
Gly Ala Ser Gly Arg Ser Val Leu Val Thr Gly Gly Ala Gly Phe Ile
15 20 25

ggc acg cac acg gcg ctg cgc ctg ctg gag cag ggc tac ggc gtc acc	265
Gly Thr His Thr Ala Leu Arg Leu Leu Glu Gln Gly Tyr Gly Val Thr	
30 35 40 45	
gtc gtc gac aac ttc cac aac tcc gtc ccc gag gcg ctc gaa cgc gtc	313
Val Val Asp Asn Phe His Asn Ser Val Pro Glu Ala Leu Glu Arg Val	
50 55 60	
cgc ctc atc gcc ggg ccc gcg ctc tcc gcc cgc ctc gac ttc atc cgg	361
Arg Leu Ile Ala Gly Pro Ala Leu Ser Ala Arg Leu Asp Phe Ile Arg	
65 70 75	
ggg gat ctg agg agc gcc ggg gac ttg gag aag gcg ttc gcg gcc agg	409
Gly Asp Leu Arg Ser Ala Gly Asp Leu Glu Lys Ala Phe Ala Ala Arg	
80 85 90	
agg tac gac gcc gtc gtc cac ttc gcg ggg ctc aag gcc gtc ggg gag	457
Arg Tyr Asp Ala Val Val His Phe Ala Gly Leu Lys Ala Val Gly Glu	
95 100 105	
agc gtc gcg cgc ccg gac atg tac tac gag aac aac ctc gcc ggc acc	505
Ser Val Ala Arg Pro Asp Met Tyr Tyr Glu Asn Asn Leu Ala Gly Thr	
110 115 120 125	
atc aac ctc tac aag gcc atg aac gag cac ggc tgc aag aag atg gtg	553
Ile Asn Leu Tyr Lys Ala Met Asn Glu His Gly Cys Lys Lys Met Val	
130 135 140	
ttc tcg tcg tcc gcg acc gtg tac ggc tgg ccg gag gtg atc ccg tgc	601
Phe Ser Ser Ser Ala Thr Val Tyr Gly Trp Pro Glu Val Ile Pro Cys	
145 150 155	
gtc gag gac tcc aag ctg cag gcc gcc aac ccc tac ggc agg acc aag	649
Val Glu Asp Ser Lys Leu Gln Ala Ala Asn Pro Tyr Gly Arg Thr Lys	
160 165 170	
ctc atc ctg gag gag ttg gcg cgg gac tac cag cgc gcg gac ccg ggc	697
Leu Ile Leu Glu Glu Leu Ala Arg Asp Tyr Gln Arg Ala Asp Pro Gly	
175 180 185	
tgg agc atc gtc ctg ctg cgc tac ttc aac ccc atc ggc gcc cac agc	745
Trp Ser Ile Val Leu Leu Arg Tyr Phe Asn Pro Ile Gly Ala His Ser	
190 195 200 205	
tcc ggc gag atc ggc gag gac ccc aag ggg gtg ccc aac aac ctg ctg	793
Ser Gly Glu Ile Gly Glu Asp Pro Lys Gly Val Pro Asn Asn Leu Leu	
210 215 220	
ccc tac atc cag cag gtc gcc gtc ggc agg ctc ccc gag ctc aac gtc	841
Pro Tyr Ile Gln Gln Val Ala Val Gly Arg Leu Pro Glu Leu Asn Val	

225	230	235	
tac ggc cac gat tac ccc acc cgt gac ggc acc gcg atc agg gac tac			889
Tyr Gly His Asp Tyr Pro Thr Arg Asp Gly Thr Ala Ile Arg Asp Tyr			
240	245	250	
ata cac gtc gtc gac ctg gcc gac ggg cac atc gcg gcg ctg aac aag			937
Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Asn Lys			
255	260	265	
ctg ttc gac act cct gat ttc ggt tgt gtg gcc tac aat ctg ggc aca			985
Leu Phe Asp Thr Pro Asp Phe Gly Cys Val Ala Tyr Asn Leu Gly Thr			
270	275	280	285
ggg cgc ggc aca tcc gtt ctg gag atg gtg gcg gcg ttc aag aag gca			1033
Gly Arg Gly Thr Ser Val Leu Glu Met Val Ala Ala Phe Lys Lys Ala			
290	295	300	
tcc ggc aag gag atc ccc acc aag atg tgc ccc agg aga ccg ggt gac			1081
Ser Gly Lys Glu Ile Pro Thr Lys Met Cys Pro Arg Arg Pro Gly Asp			
305	310	315	
gcg acg gag gtt tac gcg tcc act gag aag gcc gaa agg gag ctg gga			1129
Ala Thr Glu Val Tyr Ala Ser Thr Glu Lys Ala Glu Arg Glu Leu Gly			
320	325	330	
tgg agg gcc cag tat gga atc gag gag atg tgc agg gac cag tgg aac			1177
Trp Arg Ala Gln Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln Trp Asn			
335	340	345	
tgg gcc aag aag aac ccc tat ggc tac tgc gcc act gcc gaa aaa			1222
Trp Ala Lys Lys Asn Pro Tyr Gly Tyr Cys Gly Thr Ala Glu Lys			
350	355	360	
tagagcgcgt gcattaatca gatctctgga ctgaatttgt ccatgggttga tggttgtctc			1282
agacctatcg gtggaagatg taacaagtag agaccgctcg aatgtgccta gctacgaaag			1342
tttcgtacca tctctcttgt cataacctca tgtagatggg cattttattg gaattagcct			1402
tagccttcag gcccggcgct gttagccatt gcttgctatc gaggtaggtg gggttggaac			1462
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 <212> PRT
 <213> Seashore Paspalum

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Gly Arg Ser Val Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Thr His
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Thr Ala Leu Arg Leu Leu Glu Gln Gly Tyr Gly Val Thr Val Val Asp
35 40 45

Asn Phe His Asn Ser Val Pro Glu Ala Leu Glu Arg Val Arg Leu Ile
50 55 60

Ala Gly Pro Ala Leu Ser Ala Arg Leu Asp Phe Ile Arg Gly Asp Leu
65 70 75 80

Arg Ser Ala Gly Asp Leu Glu Lys Ala Phe Ala Ala Arg Arg Tyr Asp
85 90 95

Ala Val Val His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Val Ala
100 105 110

Arg Pro Asp Met Tyr Tyr Glu Asn Asn Leu Ala Gly Thr Ile Asn Leu
115 120 125

Tyr Lys Ala Met Asn Glu His Gly Cys Lys Lys Met Val Phe Ser Ser
130 135 140

Ser Ala Thr Val Tyr Gly Trp Pro Glu Val Ile Pro Cys Val Glu Asp
145 150 155 160

Ser Lys Leu Gln Ala Ala Asn Pro Tyr Gly Arg Thr Lys Leu Ile Leu
165 170 175

Glu Glu Leu Ala Arg Asp Tyr Gln Arg Ala Asp Pro Gly Trp Ser Ile
180 185 190

Val Leu Leu Arg Tyr Phe Asn Pro Ile Gly Ala His Ser Ser Gly Glu
 195 200 205

Ile Gly Glu Asp Pro Lys Gly Val Pro Asn Asn Leu Leu Pro Tyr Ile
 210 215 220

Gln Gln Val Ala Val Gly Arg Leu Pro Glu Leu Asn Val Tyr Gly His
 225 230 235 240

Asp Tyr Pro Thr Arg Asp Gly Thr Ala Ile Arg Asp Tyr Ile His Val
 245 250 255

Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Asn Lys Leu Phe Asp
 260 265 270

Thr Pro Asp Phe Gly Cys Val Ala Tyr Asn Leu Gly Thr Gly Arg Gly
 275 280 285

Thr Ser Val Leu Glu Met Val Ala Ala Phe Lys Lys Ala Ser Gly Lys
 290 295 300

Glu Ile Pro Thr Lys Met Cys Pro Arg Arg Pro Gly Asp Ala Thr Glu
 305 310 315 320

Val Tyr Ala Ser Thr Glu Lys Ala Glu Arg Glu Leu Gly Trp Arg Ala
 325 330 335

Gln Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln Trp Asn Trp Ala Lys
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Lys Asn Pro Tyr Gly Tyr Cys Gly Thr Ala Glu Lys
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<220>
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atctccatct cccaccccca tcgatccatt tgtgttggt ttaattccct gcgtgcatgc 180
gtgttggtga ataagggggc ggttccatct gtacgtacgt gtactccgag acctatcgtc 240
atgtgtgtgt gtgtacgtat acctgctgtg tacatgatgg tcgtatatgc cactggacta 300
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<212> DNA
<213> Seashore Paspalum

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aaatagagcg cgtgcattaa tcagatctct ggactgaatt tgtccatggt tgatggttgt 120
ctcagaccta tcggtggaag atgtaacaag tagagaccgc tcgaatgtgc ctagctacga 180

agtttcgtac catctctctt gtcataacct catgtagatg gtcattttat tggaattagc	240
cttagccttc aggcccggcg ctgttaaaat ttgttttaca catggatttt ctcgctacgt	300
gtgatacata ttgtgtctgt aataatcctg atcggagttt ccagtaataa aaccgatcca	360
cgacggtggc tacgccctgt gttgtagtac tgtgaatatg atgtggtaat aacaataact	420
tgcagtgaga cttcagcttt caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	480
aaaaaaaaaa aaaaaaa	497

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ctgccgaaaa atagagcgcg tgcattaatc agatctctgg actgaatttg tccatgggtg	120
atggttgtct cagacctatc ggtggaagat gtaacaagta gagaccgctc gaatgtgcct	180
agctacgaag ttctgtacca tctctcttgt cataacctca thtagatggg cattttattg	240
gaattagcct tagccttcag gcccggcgct gttaaaattt gttttacaca tggattttct	300
cgctacgtgt gatacatatt gtgtctgtaa taatcctgat cggagtttcc agtaataaaa	360
ccgatccacg acggtggcta cgccctgtgt tgtagt	396

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<220>
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 <222> (110)..(1183)

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agcctttcct tccccgatcg ccgatccgat ccacaagcaa gcagccagg atg gtt tct	118

Met Val Ser

1

gcg	gtg	ctt	cgt	acc	atc	ctt	gtg	acg	ggc	ggc	gcc	ggc	tac	atc	ggc	166
Ala	Val	Leu	Arg	Thr	Ile	Leu	Val	Thr	Gly	Gly	Ala	Gly	Tyr	Ile	Gly	
5						10					15					
agc	cac	acc	gtg	ctg	ctg	ctg	ctg	cag	cag	gga	ttc	cgc	gtc	gtc	gtc	214
Ser	His	Thr	Val	Leu	Leu	Leu	Leu	Gln	Gln	Gly	Phe	Arg	Val	Val	Val	
20				25						30					35	
gtc	gac	aac	ctc	gac	aac	gcc	tcc	gac	gtc	gcg	ctc	gcc	cgc	gtc	gcg	262
Val	Asp	Asn	Leu	Asp	Asn	Ala	Ser	Asp	Val	Ala	Leu	Ala	Arg	Val	Ala	
			40						45					50		
cag	ctc	gca	gca	agc	agc	aac	ggc	ggc	gcc	gcc	aac	ctc	gtc	ttc	cac	310
Gln	Leu	Ala	Ala	Ser	Ser	Asn	Gly	Gly	Ala	Ala	Asn	Leu	Val	Phe	His	
		55					60						65			
aag	gtt	gac	ctt	cgc	gac	agg	cac	gcg	ctg	gag	gac	atc	ttc	tcc	tcc	358
Lys	Val	Asp	Leu	Arg	Asp	Arg	His	Ala	Leu	Glu	Asp	Ile	Phe	Ser	Ser	
	70						75					80				
cac	agg	ttt	gag	gct	gtg	att	cat	ttt	gct	ggg	ctc	aaa	gct	gtt	ggc	406
His	Arg	Phe	Glu	Ala	Val	Ile	His	Phe	Ala	Gly	Leu	Lys	Ala	Val	Gly	
85						90					95					
gag	agc	gtg	cag	aag	ccg	ctg	ctt	tac	tac	gac	aac	aac	ctc	atc	ggc	454
Glu	Ser	Val	Gln	Lys	Pro	Leu	Leu	Tyr	Tyr	Asp	Asn	Asn	Leu	Ile	Gly	
100					105					110					115	
acc	atc	acc	ctc	ctc	gag	gtc	atg	gcc	gca	cat	ggc	tgc	aag	aag	ctg	502
Thr	Ile	Thr	Leu	Leu	Glu	Val	Met	Ala	Ala	His	Gly	Cys	Lys	Lys	Leu	
				120					125					130		
gtg	ttc	tcg	tca	tct	gca	act	gtc	tat	ggg	tgg	ccc	aag	gaa	gtg	cca	550
Val	Phe	Ser	Ser	Ser	Ala	Thr	Val	Tyr	Gly	Trp	Pro	Lys	Glu	Val	Pro	
			135					140					145			
tgc	acc	gaa	gaa	ttc	cct	ctt	tgc	gcc	acc	aac	ccc	tat	ggg	cga	acc	598
Cys	Thr	Glu	Glu	Phe	Pro	Leu	Cys	Ala	Thr	Asn	Pro	Tyr	Gly	Arg	Thr	
		150					155					160				
aag	ctt	gtg	att	gaa	gat	atc	tgc	cgc	gac	gtc	cac	cgt	tca	gac	cct	646
Lys	Leu	Val	Ile	Glu	Asp	Ile	Cys	Arg	Asp	Val	His	Arg	Ser	Asp	Pro	
	165					170					175					
gat	tgg	aag	atc	ata	ctg	ctc	agg	tac	ttc	aac	cct	gtt	ggt	gct	cat	694
Asp	Trp	Lys	Ile	Ile	Leu	Leu	Arg	Tyr	Phe	Asn	Pro	Val	Gly	Ala	His	
180					185					190					195	

cca agc gga cac atc ggt gaa gac ccc tct gga atc cca aac aac ctg	742
Pro Ser Gly His Ile Gly Glu Asp Pro Ser Gly Ile Pro Asn Asn Leu	
200 205 210	
atg ccc tat gtc cag caa gtt gcc gtt ggg agg agg cct cac ctc act	790
Met Pro Tyr Val Gln Gln Val Ala Val Gly Arg Arg Pro His Leu Thr	
215 220 225	
gtc tat gga acc gac tac aac aca aag gat gga act ggg gtg cgc gat	838
Val Tyr Gly Thr Asp Tyr Asn Thr Lys Asp Gly Thr Gly Val Arg Asp	
230 235 240	
tat atc cat gtt gtt gac ctg gcc gat ggg cac ata gca gcc ctg ggg	886
Tyr Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Gly	
245 250 255	
aag ctc tat gaa gac tct gac aga ata ggg tgt gag gta tac aac ctg	934
Lys Leu Tyr Glu Asp Ser Asp Arg Ile Gly Cys Glu Val Tyr Asn Leu	
260 265 270 275	
ggc aca gga aag ggg act tcg gtg ctg gaa atg gtg gct gca ttc gag	982
Gly Thr Gly Lys Gly Thr Ser Val Leu Glu Met Val Ala Ala Phe Glu	
280 285 290	
aag gtt tct ggc aag aaa atc cct ctg gtg ctt gct ggg cga aga cct	1030
Lys Val Ser Gly Lys Lys Ile Pro Leu Val Leu Ala Gly Arg Arg Pro	
295 300 305	
gga gat gca gag att gtt tat gct gca act gcc aag gcc gag aaa gag	1078
Gly Asp Ala Glu Ile Val Tyr Ala Ala Thr Ala Lys Ala Glu Lys Glu	
310 315 320	
ctg aaa tgg aag gcc aag tac ggg att gaa gag atg tgc aga gac cag	1126
Leu Lys Trp Lys Ala Lys Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln	
325 330 335	
tgg aac tgg gca agc aaa aac ccc tac ggg tat gct gga tca ccc gac	1174
Trp Asn Trp Ala Ser Lys Asn Pro Tyr Gly Tyr Ala Gly Ser Pro Asp	
340 345 350 355	
aac agc agc tgactgaaag caaatgcatg ctatgcatga tagggagatc	1223
Asn Ser Ser	
gagcagcaga ccacttacca ctgctagtaa aagaagtcca gtctcagaat accaccgtac	1283
gatatgcttac taaatagtcc gaggacggac ggacggatga tccatgtgtg gggcctcgta	1343
ttctcatttg tatagaggga cggagtagga gatccccagt cccatccatc cggcttattg	1403
ttgctaccgt caatccatgt ttaagaaata aaccctatg catgtatgct tatcgatcta	1463

ctgtactagc taattatata ggcataatgta tatttggttag attccttatac aaaaaaaaaa 1523

aaaaaaaaaa aaaaaaa 1540

<210> 9

<211> 358

<212> PRT

<213> Seashore Paspalum

<400> 9

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Val Val Val Val Asp Asn Leu Asp Asn Ala Ser Asp Val Ala Leu Ala
35 40 45

Arg Val Ala Gln Leu Ala Ala Ser Ser Asn Gly Gly Ala Ala Asn Leu
50 55 60

Val Phe His Lys Val Asp Leu Arg Asp Arg His Ala Leu Glu Asp Ile
65 70 75 80

Phe Ser Ser His Arg Phe Glu Ala Val Ile His Phe Ala Gly Leu Lys
85 90 95

Ala Val Gly Glu Ser Val Gln Lys Pro Leu Leu Tyr Tyr Asp Asn Asn
100 105 110

Leu Ile Gly Thr Ile Thr Leu Leu Glu Val Met Ala Ala His Gly Cys
115 120 125

Lys Lys Leu Val Phe Ser Ser Ser Ala Thr Val Tyr Gly Trp Pro Lys
130 135 140

Glu Val Pro Cys Thr Glu Glu Phe Pro Leu Cys Ala Thr Asn Pro Tyr
145 150 155 160

Gly Arg Thr Lys Leu Val Ile Glu Asp Ile Cys Arg Asp Val His Arg
165 170 175

Ser Asp Pro Asp Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val
180 185 190

Gly Ala His Pro Ser Gly His Ile Gly Glu Asp Pro Ser Gly Ile Pro
195 200 205

Asn Asn Leu Met Pro Tyr Val Gln Gln Val Ala Val Gly Arg Arg Pro
210 215 220

His Leu Thr Val Tyr Gly Thr Asp Tyr Asn Thr Lys Asp Gly Thr Gly
225 230 235 240

Val Arg Asp Tyr Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala
245 250 255

Ala Leu Gly Lys Leu Tyr Glu Asp Ser Asp Arg Ile Gly Cys Glu Val
260 265 270

Tyr Asn Leu Gly Thr Gly Lys Gly Thr Ser Val Leu Glu Met Val Ala
275 280 285

Ala Phe Glu Lys Val Ser Gly Lys Lys Ile Pro Leu Val Leu Ala Gly
290 295 300

Arg Arg Pro Gly Asp Ala Glu Ile Val Tyr Ala Ala Thr Ala Lys Ala
305 310 315 320

Glu Lys Glu Leu Lys Trp Lys Ala Lys Tyr Gly Ile Glu Glu Met Cys
325 330 335

Arg Asp Gln Trp Asn Trp Ala Ser Lys Asn Pro Tyr Gly Tyr Ala Gly
340 345 350

Ser Pro Asp Asn Ser Ser

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<223> Synthetic DNA

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<210> 11
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<212> DNA
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<210> 17
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ttgttctcgt acatgta

17